

[illegible]

Query Match 35.7%; Score 425; DB 9; Length 966;
Best Local Similarity 65.4%; Pred. No. 1.7e-124;
Matches 623; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

Qy 230 TTGGAAATTCCATCTTACATCGAGCCGCCGAAGCATACAAAATCCGTTCACTCGTA 289

```
Db 7 TTGCGAAAAACGATGATCAGATGATCCGCGGAAACACACGAGAAATCAGATCGATCGTCA 66
Qy 290 ACAAGCCTTTACTCCGCGGTGATGAAGCAATGGGAACCGAGAAATTCAGAAATCACAG 349
Db 67 ACAAGCCTTTTACCGCGCGTATGAAGAGTGGGAGCGCGCATTCGCGAACTGACGA 126
Qy 350 ATGAACCTGATTCAAAATTTTCAGGCGCGAGTGAGTTTGACCTTGTTCACGATTTTTCAT 409
Db 127 ATCAATGCTCGTGATGTCGCGGAGGAGAGATCGACCTTGTACAGGATTTTTCAT 186
Qy 410 ACCCGCTCCCGTATTGTGATATCTGAGCTGCTGGAGTGCCTTCAGCGAGATGGAAC 469
Db 187 ATCCGTTGCCGCTAATCGTCATTTCCGAATTCGTCGCGTTCCTTTGGTGATAGCATC 246
Qy 470 AGTTTAAACAGTGTCTGATCTTCTGTCAGTACACCGGAAGGATAAAGTGAAGAGCTG 529
Db 247 ATTTTCAAGAAATGCTCCGACCTGTGTGTCAGCTCCGGAAGAGCGATCGCGCGAAGATG 306
Qy 530 AAAAAGCCTTTTGGAAAGAACAGATAAGTGTGAGGAAGAACTGGCGCGGTTTTTTGCCG 589
Db 307 TGAACGAGTGGAAAAACATCAGGACCAAGGCGGAGAGAGCTGACCGCATCTTTGAAA 366
Qy 590 GCATCATAGAAGAAAGCGAAACAAACCGGAACAGAGATATTATTTCTATTTTAGTGAAG 649
Db 367 AGATGATTGAAGAGAAAGACAAAACCTCGGCAATGACCTGATTTTCGCTTTTGATCAAG 426
Qy 650 CGGAGAAACAGCGAGAGAGCTGTCGGGTGAAGAGCTGATTCGGTTTTGACGCTGCTGC 709
Db 427 CGGAACAAAGAGGGAACAGCTGTCCCTCTGATGAATTTGGTTCCATTTTGCATCTGCTCT 486
Qy 710 TGTGTGCGCGGAATGAAACCACTACAAACCTGATTTCAAATGCGATGATCAGCATATTAG 769
Db 487 TGAATGCGCGGGAATGAACGACGCAATTTAGTTTCAAATGGGCTTACAGCATTTCTCG 546
Qy 770 AAAACCGCAGCGCTTTACGAGGAACCTCGCAGCGCATCTCGAACTGATGCTCTAGCGAGTGG 829
Db 547 AAACACCGGCGGTGATGACGAGCTCGCAGGCGATCTCGAACTGATTCGCGAGGAGTGG 606
Qy 830 AGGAGCCTTGGCTTTACAGCGCGCGCGCGCTTTTGGGCGCATTTGCCAAGCGGATA 889
Db 607 AGGAAGCGCTCGCTTTCCGGGCGCGAGCGCGGATGATGTGCGCTTCGTTTAAACAGGATA 666
Qy 890 CGGAGATCGGGGGCACCTGATTTAAAGAGAGTGATATGCTTTTGGCGTTTGTGGCATCGG 949
Db 667 CCGAGATCAGAGAGTAACTGTAAGAAAAGGAGAGGTGTGATCGCTTTCTTGTCTCTG 726
Qy 950 CAAATCGTGATGAAGCAAAAGTTTGAACAGCGCAGATTTTGATATCCGCGCGCATCCCA 1009
Db 727 CCAACCGTGATGAACGAAATTTGAGAGGCGCGCACGAAATTTGATATTACCGCGCATCCGA 786
Qy 1010 ATCCGCAATTCGCTTTGGCCAGCGCATCCATTTTTCCTTGGGCGCGCGCTTGGCCGTC 1069
Db 787 ACCCGCATATCGGATTTGGGACGGCATCCACTTTTGTGGGCGCGCGCTCGCAAGGC 846
Qy 1070 TTGAACAAATATCGGTTTAAACGTCCTTTGATTTCTGCTTTTCTCATATGGAGTGGTCA 1129
Db 847 TGAACCGCGCATCGCATTTAGGCGCTCTTAAAGCAGTATGCCTCGATGGAAAGCTTG 906
Qy 1130 GTATCACTCCGATTGAAAACAGTGTGATATACGATTAAGAGCTTTCGCTGTG 1182
Db 907 CGGTCTGTCGATGGCGGACAGCAGCATGTACGGCTTTGAAACATTTCCGCTCTG 959
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RESULT 2

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US-09-974-300-2182
; Sequence 2182, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
```

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; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2182
; LENGTH: 1213
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-2182
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Query Match 20.3%; Score 242; DB 9; Length 1213;
Best Local Similarity 53.6%; Pred. No. 7.2e-66;
Matches 550; Conservative 0; Mismatches 470; Indels 6; Gaps 2;
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Qy 75 TCCGTTTCCATGGTATGAATCGATGAGAAAGGATGCGCTCTTTCTTTGATGAAGAAAA 134
Db 92 TCCGTTTCCGATTTATAACCGGATCAGAAAGACGTCCTCTGCGTTACGATGATGAGCG 151
Qy 135 CCAAGTGTGGAGCGTTTTTCTTTATGATGATGTCAAAAAAGTTGTGGGGATAAAGATT 194
Db 152 AAAATGCTTTGATATCTTTTCTTATGAAGAGCTTCAATTCGTGTAAAAAACCCTGAAGCT 211
Qy 195 GTTTTCCAGTTGCTATGCGCGAGCAGACAAGCTCTATTGGAAATTCATCATTTACATGGA 254
Db 212 CTTCTC-----TTCAAAACGCGCGGTAAATGGAA--GGAAAAAGTATTATTAACAATGGA 265
Qy 255 CCGCGGGAAGCATACAAAATCCGTTCACTGCTGTAACAAAGCCTTTTATCTCCGCGGTGAT 314
Db 266 CCGCGGAGACACACAAAATGAGAGCCATCGTTAATAAGCTTTTACCGCGGAAGCGGT 325
Qy 315 GAAGCAATGGAAACGAGAAATTCAGAAATCACAGATGAACTGATTTCAAAATTTTCAGGG 374
Db 326 GAAAGAGCTTGAACCGCATATCGAAGAGTGCAGCGCTTTTATTTAAACGAAGCGAAACA 385
Qy 375 GCGCAGTGAGTTTGACCTTTGTTTACGATTTTATACCGCTTCGGTTATTGTGATATC 434
Db 386 GAAAGAAATGTTGATGTTGGTGGAGACTTGGCTGCTCTCTCCCGTCATTTATCATCGC 445
Qy 435 TGAGCTGCTGGGAGTGCCCTTCAGCGCAGATGGAAACAGTTTAAAGCATGGTCTGATCTTCT 494
Db 446 TGAACCTTTTAGCGCTTCGCGCTGAAGACCGCTCATGTTTAAACATTTATTCAGACATCCT 505
Qy 495 GGTCAGTACACGGAAGGATAAAGTGAAGAGCTGAAAAAGCCTTTTGGGAAGAACGAGA 554
Db 506 TGTGCGAGTGGGAAGACCGCTCGGCTGAAGCGCGCGAGCGGATGTACAAAACGACGTGA 565
Qy 555 TAAAGTGTGAGGAAGAACTGGCGCGGTTTTTTTGGCGCATCATAGAAGAAAAAGCGAAACA 614
Db 566 AAGAGGCAATCGGTTTTTGGCGGATATTATTTAAACATTTATCAAGAGCGCAAAAAGA 625
Qy 615 ACCGGAAACAGGATATTATTTCTATTTTAGTGAAGCGGAAGAAACAGCGGAGAAAGCTGC 674
Db 626 GCCAAAACAGCAGCTGATTTTCGCTTTTACTCGGCGGAGTGTGAGCGCAAAATCGCTGAC 685
Qy 675 CGGTGAAGAGCTGATTCGTTTTTGGACCGCTGCTGTGTGGCGCGGAATTAAGAACCACTAC 734
Db 686 AGAAGAAACTGCTTTCATTTTTCATTTTGGTTCGAGGCAATGAGACGACAAC 745
Qy 735 AAACCTGATTTCAAATGCGATGTACAGCATATTAGAAACGCGCGGTTTTACGAGGAACT 794
Db 746 CAATTTGATCGCAACAGCGTCCGCTATCTCACAGAGATTAATATCACAGGAAGCCGT 805
Qy 795 GCGCAGCCATCTCGAACTGATGCCTTCAGCGAGTGGAGGAAGCCTTTGCGTTTTCAGAGCGCC 854
Db 806 AAGCAAGATCGTCCCTCGTCTCTTTGTTGAAGAAATGCTGCGTTATTATTCGCGC 865
Qy 855 GCGCCCGTTTTAGGCGCATTTGCCAAGCGGATACGAGATCGGGGGCACCTGATTAA 914
Db 866 CGTCAAGCGATCGGCGCGCACGCGGCGAGAGACGTTGATATCGGAGCGGTGAGGATGC 925
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QY 539 TTTTGAAGAACGAGATAAGTGTGAGGAAGAACTGGCGCGGTTTTTTTTCGGGCATCATAG 598
Db 3308 TCACCGAGAGCGTGGCGCCGCGCATCTGAGGAGTGTTCGGAATCTCTTAAGCCGAGATCG 3249
QY 599 AAGAAAGCGAAACAAACCGGAACAGGATATTTATTTCTATTTTATGTAAGCGGAAGAAA 658
Db 3248 CCCACAAGCGCGCCGAAACCGAAGGACGACCTGATCAGCGGCGCTCTGTGCGCGGAGGTCTG 3189
QY 659 CAGCGGAGAGCTGTCGCGTGAAGAGCTGATTCCTGTTTTTGACGCTGCTGTGTTGGCGG 718
Db 3188 ACGGCGGCAAGCTGACCGAGGAGGAGTGTCAACATGCTGCGCTGTCTCACCGCGG 3129
QY 719 GAAATGAACAACTACAAACCTGATTTCAATGCGATGTACAGCATATTTAGAAAACGCCAG 778
Db 3128 GGCATCTCCAGCGCCAGCTGCTCAGCAACCTGTCTCTGTGCTGGAGGACCCGCG 3069
QY 779 GCGTTTACGAGAACTGGCGACCCATCTGAACTGATGCTCAGGACGTGGAGGAGGCT 838
Db 3068 AGGCACAGCGCGGTTCGCGCGGACCGCAGCTCTGTGCGGCGTGTATCGAGGAGACGC 3009
QY 839 TCGGTTTACAGCGCGCGCGCGGTTTTTGAGGCGCATTCGCAAGCGGATACGGAGATCG 898
Db 3008 TCGGTTTACCGGTCGCGGTTCAACTGCACTTCCGATCTTGAACGAGGACACCGCATCC 2949
QY 899 GGGGCGACCTGATTAAGAAAGGTGATATGTTTTTGGCGTTTTGTGCGCATCGGCAAACTCGTG 958
Db 2948 TCGGCGCACCCATGCGCAAGGCGCAGATGTTGATCGCTTGGATCGCTCCGCGAACCAG 2889
QY 959 ATGAAGCAAAAGTTGACAGACCGCATGTTTTGATATCGCGCGCATCCCAATCCGCATA 1018
Db 2888 ACACCGAGGTGTTACCGGACCCGACACCTTCGACATCGACGCGGAGTCGAACAAGCACC 2829
QY 1019 TTGCGTTTGGCCACGGCATCAATTTTGGCTTTGGGCGCGCGTTGCGCGTCTTTGAAGCA 1078
Db 2828 TGGCGTTTGGCCACGGCATCAATTTTGGCTTTGGGCGCGCGTTGCGCGTCTTTGAAGCA 2769
QY 1079 ATATC 1083
Db 2768 AGGTC 2764

RESULT 5

US-10-156-761-576
; Sequence 576, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 576

; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1197)
US-10-156-761-576

Query Match

11.4%; Score 135.4; DB 15; Length 1197;

Best Local Similarity 48.9%; Pred. No. 9.5e-32;
Matches 364; Conservative 0; Mismatches 381; Indels 0; Gaps 0;
QY 344 TCACAGATGACTGATTCATAAAATTTTCAGGCGCGCAGTGTGACCTTGTTCACGATT 403
Db 347 TGACAAGGAACTGGCGAAGTGTTCAGGAGGCGAGCAGATCGATCGTGTGACGACT 406
QY 404 TTTTATATCCCGCTTCCGCTTATTTGTGATATCTGAGCTGCTGGGAGTGCCTTTCAGCGCAGA 463
Db 407 TCGCTTACCACTGCGCGTGAACCGTGTCTGCGCCTGCTCGGCATCCCGACAAGGACG 466
QY 464 TGGAACTAGTTTAAAGCATGTCTGATCTTCTGGTCTAGTACACCGAAGATATAAGTGAAG 523
Db 467 AGCAGCTCTTCCAGGACTGGACCATACCTCTGCTGCGTCCGCGACATCCGCGCCCGAAG 526
QY 524 AAGCTGAAAAAGCCCTTTTGGAAACACGAGATAAGTGTGAGGAAGAACTGCGCGCTTTT 583
Db 527 GTGACACCGCGAAACGGGACCCAGCGCGCCAGCAGGCGCAGCAGAGATGGGCGCAGTACC 586
QY 584 TTGCGCGCATCATAGAAAGAAAGCGAAACAAACCGGAACAGGATATTTATTTTATTTTAG 643
Db 587 TGGTCCAACCTGCGCAACAGCGCGCGGTGGGCGCCACCGGCGACATGCTCTCCGACCTCG 646
QY 644 TGGAAAGCGGAAGAAACAGGCGGAGAAAGTGTCCGCTGAAGAGCTGATTCGCTTTTGCAGCG 703
Db 647 TCAACGAACCGGACCCCGCGCGACGGCTCAGCGAGGAGGACCTGGCGCGCAACACCATCC 706
QY 704 TGCTGCTGGTGGCGGGAATGAACCACTACAAACCTGATTTCAAAATGCGATGTACAGCA 763
Db 707 TGCTGTTTCAATCGCGCGACACGAGACCACTGATCTGATCGCAACCGCGCTCTCACCC 766
QY 764 TATTAGAAACCGCAGGCGGTTTTACGAGGAACCTGCGCAGCCATCTCTGAACCTGATGCTCAGG 823
Db 767 TGTGGCGCGCGCGCAACCACTGACCGCTCTGCGGGAAGACCCCGAGCTGTGCGCGAG 826
QY 824 CAGTGGAGGAAGCTTGTGCTTTTACAGCGCGCGCGCGCGGTTTTTGAAGGCGCATTTGCCAAGC 883
Db 827 CGGTGGAGAACTGCTGCGCTACGAGCGCGCGTCCACATCGCGAGCGGGTTCCTCCCTCG 886
QY 884 GGGATACGAGATCGGGGGGCACTGATTAAGAAGGTGATATGTTTGGCGTTTGTGG 943
Db 887 TCGACATCGAGCTGCGCGGCGCACCGATCCCGGTGGCACGCTCCGTCACTCTGGCGCTGG 946
QY 944 CATCGCAAAATCGTGATGAAGCAAAAGTTTGAACAGCGCACATGTTTGATATCGCGCGCC 1003
Db 947 CCTCGGCGAGCGCGACCCGATGCGGTTTACGCGAACCCGAGTTCGACCCACCCGCGCC 1006
QY 1004 ATCCCAATCCGCATATTGCGTTTGGCCACCGGCATCCATTTTGGCTTGGGCGCGCGCTTG 1063
Db 1007 CGGACAACCGACGCTGCGCTTCGGCAGCGGTATCCACCTGTGCTTTCGGCGCGCCACTCG 1066
QY 1064 CCGCTCTTGAAGCAAAATATCGCGTT 1088
Db 1067 CCGTATCGAAGCGGCGCGCGCT 1091

RESULT 6

US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089

;; PRIOR FILING DATE: 2001-05-30
;; PRIOR APPLICATION NUMBER: JP 2001-272697
;; PRIOR FILING DATE: 2001-08-02
;; NUMBER OF SEQ ID NOS: 15109
;; SEQ ID NO 1
;; LENGTH: 9025608
;; TYPE: DNA
;; ORGANISM: Streptomyces avermitilis
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (4187715)
;; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 11.4%; Score 135.4; DB 15; Length 9025608;
Best Local Similarity 48.9%; Pred. No. 3e-29;
Matches 364; Conservative 0; Mismatches 381; Indels 0; Gaps 0;

Qy 344 TCACAGATGAAGTAAAGCAATTTCAAGGGCGCAGTGTGACCTTGTTCACGATT 403
Db 737658 TGACCAAGGAAGTGGCGGAAGTGTTCAGGAGGGCAGGCAGATCGTCGACGACT 737717

Qy 404 TTTTCATCCCGCTTCCCGTATTGTGATATCTGAGCTGCTGGAGTGCTTTCAGCGCAGA 463
Db 737718 TCGCTTACCCACTGCGCGTGACCGTGATCTCGCGCTGCTCGGATCCCGGACAAGACG 737777

Qy 464 TGGAAACAGTTAAAGCATGTCTGATCTTCTGTGTCAGTACACCGAAGGATAAAAGTGAAG 523
Db 737778 AGCAGCTTCTCCAGGACTGGACCGATACCTCTGTCGGTCCGCGACATCGGGCCCGAAG 737837

Qy 524 AAGCTGAAAAAGCCTTTTGGGAAGAACCGAGATATAGTGTGAGGAAGAACTGGCCCGGTTTT 583
Db 737838 GTGACACCGCGAAGCGGACCGCGCGCCAGCCAGCGGCGCAGCAGAGATGGCGCAGTACC 737897

Qy 584 TTGCGCGCATCATAGAACAAAGCGAACAACCGGACAGATATTTCTATTATTAG 643
Db 737898 TGGTCCAACTCGCGAAGACGGCGCGGTGTCGGCCACCGCGGACATGCTCTCCGACCTCG 737957

Qy 644 TGGAAAGCGGAAGAAACAGCGGAGAGTGTCTCGGTGAAGAGCTGATTCGGTTTTTGCACGC 703
Db 737958 TCAACGAACCGGACCGCGCGCGACCGCTCAGGAGGAGGACCTGGCGGGAACACCATCC 738017

Qy 704 TGCTGTGTTGGCGGGAATGAAACCACTA CAACCTGATTTCAAAATGCGATGTACAGCA 763
Db 738018 TGCTGTTTCATCGCGGACACGAGACCAACGCTCAATCTGATCGCAACCGGCTCCTCACCC 738077

Qy 764 TATTAGAAACCGCAGGCGTTTACGAGGAACTGCGCAGGCCATCTTGAACGTGATGCTCAGG 823
Db 738078 TGTTCGCGCGCGCGACCAACTGAGACCGTCTGCGGGAAGACCCAGCGCTGTCGCGCGAG 738137

Qy 824 CAGTGGAGAGACCTTGGGTTTTCAGAGCGCGCGCGCGGTTTTCAGGGCGCATTCGCCAAGC 883
Db 738138 CGGTGGAGAACTGCTGCGCTACGAGCCCGCGTCCACATCGCGGAGCGGGTCCCTCTCG 738197

Qy 884 GGGATACGGAGATCGGGGGCACCCTGATTAAGAAAGGTGATATGTTTGGCGTTTGTGG 943
Db 738198 TCGACATCGATCGCGCGCACCAAGATCCCGCGTGGCAGCTCGCTCATCTGCGGCTGG 738257

Qy 944 CATCGGCAAAATCGTGATGAACAAAGTTTGACAGCCGACATGTTTGATATCGCGGCC 1003
Db 738258 CCTCGGCGAGCGCGGACCCGATGCGGTTTCAGCAACCCGACCGGTTCGACCCCAACCGGCC 738317

Qy 1004 ATCCCAATCCGCAVATTCGGTTTGGCCACGCGATCCATTTTTTGGCTTGGGCGCCCGGTTG 1063
Db 738318 CGGACACGAGCATGCTCGGCTTGGCAGCGGTATCCACCTGTGCTTGGCGCGCACTCG 738377

Qy 1064 CCCGTCCTTGAAGCAAAATATCGCGTT 1088
Db 738378 CCCGTCGAAGCCGAGGCGCGCT 738402

RESULT 7
US-10-680-860A-23

;; Sequence 23, Application US/10680860A
;; Publication No. US20050202528A1
;; GENERAL INFORMATION:
;; APPLICANT: BLONDELET-ROUAULT, Marie-Helene
;; APPLICANT: DOMINGUEZ, Helene
;; APPLICANT: DARBON-RONGERE, Emmanuelle
;; APPLICANT: GERBAUD, Claude
;; APPLICANT: GONDRAN, Anne
;; APPLICANT: KARRAY, Fatma
;; APPLICANT: LACROIX, Patricia
;; APPLICANT: OBSTREICHER-MERMET-BOUVIER, Nathalie
;; APPLICANT: PERNODET, Jean-Luc
;; APPLICANT: TUPHILE, Karine
;; TITLE OF INVENTION: POLYPEPTIDES INVOLVED IN THE BIOSYNTHESIS OF SPIRAMYCINS, NUCLEOT
;; TITLE OF INVENTION: SEQUENCE ENCODING THESE POLYPEPTIDES AND APPLICATIONS THEREOF
;; FILE REFERENCE: FRAV2002/0028 US NP
;; CURRENT APPLICATION NUMBER: US/10/680,860A
;; 2003-10-07
;; CURRENT FILING DATE: 2003-10-07
;; PRIOR APPLICATION NUMBER: FR 0212489
;; PRIOR FILING DATE: 2002-10-08
;; PRIOR APPLICATION NUMBER: FR 0302439
;; PRIOR FILING DATE: 2003-02-27
;; PRIOR APPLICATION NUMBER: US 60/493,490
;; PRIOR FILING DATE: 2003-08-07
;; NUMBER OF SEQ ID NOS: 161
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 23
;; LENGTH: 1212
;; TYPE: DNA
;; ORGANISM: Streptomyces ambofaciens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(1212)
US-10-680-860A-23

Query Match 11.0%; Score 130.6; DB 22; Length 1212;
Best Local Similarity 48.0%; Pred. No. 3.3e-30;
Matches 404; Conservative 0; Mismatches 434; Indels 3; Gaps 1;

Qy 251 TGGACCCGCGGAGCAGTACAAAATCGTTTCAGTCGTGAACAAAGCCTTTACTCCGCGC 310
Db 257 TGGACCCGCGCGCGCAGGACCGATGCGCAAGCTGTGAGCCAGGCGTTTACCCTCCGAC 316

Qy 311 TGAATGAAGCAATGGGAACCGAGAAATCAAGAAATCAAGATGAATCAATGATTTCAAAAATTT 370
Db 317 GGATCGCGCGCTGGAGCCCGAGGTCGCGCGATCACCGAGGAGCTCTCGCAAGGTGG 376

Qy 371 AGGGGCGCAGTGTGATTTGACCTTGTTCACGATTTTTCATACCGCTTCCGGTTATTGTGA 430
Db 377 GGCAGCAGGACGTCGTGCGACCGCTGGGTGACCTGTCTACGCGCTGCGGTCATCGTGA 436

Qy 431 TATCTGAGCTGCTGGGAGTGCCTTTCAGCGCAGATGGAACAGTTTAAAGCATGTTCTGATC 490
Db 437 TCGCGGAACCTGCTGGGANTATACCGCGCGCGACCGTGACCTGTTCCGGGAGTGGGTGCA 496

Qy 491 TTCTGTGTCAGTACACCGAAGGATAAAGTGAAGAGCTGAAAAGCCTTTTGGGAAGAAC 550
Db 497 CCCTGTGTCAGCAGGAGGCTGGAGTACCCGGAACCTCCCGGACAACTTCACCGAGACGA 556

Qy 551 GAGATAAGTGTGAGGAAGAACTGCGCGCGGTTTTTTCGCGGATCATAGAGAAAGCGAA 610
Db 557 TCGCGCGCGGCTCAAGGAGATGACCGACTACCTCTGAAAGCAGATCCAGCCCAAGCGGG 616

Qy 611 ACAACCGGAACAGGATATTATTTCTATTTTCTAGTGGAGCGGAAGAACAGGCGGAGAGC 670
Db 617 ACGCGCGCGCGCGACCGACTTGGTTCAGCGGAGCAGGACCGGCGCGCGCGCGC 676

Qy 671 TGTCCGCTGAAGAGCTGATTCGCTTTTTCAGCGCTGCTGCTGGTGGCGGAAATGAAACCA 730
Db 677 TGACCGAGCTGAGATCGTCAACATCGTCCGCTGCTCTGACGCGGCGGCGACGTCCTCT 736

Qy 731 CTACAAACCTGATTTTCAATGCGATGTATAGCATATTAGAAACGCCAGCGCTTTACGAGG 790

Db	737	CCAGCACCTGCTCAGCAACCTGTTCTGCTCCTGGAGGAGAAACCGCAGGCGCTGGAGG	796
Qy	791	AACTGGCGAGCCATCCTGAACCTGATGATGCTCAGGAGAGTGGAGAAAGCCTTTCGTTTCAGAG	850
Db	797	ACCTCGCGGCGCATCGCTCCCTGGTGGCGGCGCATCGAGAGACGCTTGGCTTACCGCA	856
Qy	851	CGCCGCGCCCGTTTGGAGGCGCATTGCACAGCGGATACGAGAGATCGGGGGCACCTTGA	910
Db	857	GCCTCTTCAACAACTCTTCCGGTTCGTCAAGAGAGACACACCGTCTCTGGTCCGCTCA	916
Qy	911	TTAAGAAAGGTGATATGTTTGGCTTTGGCTTTCGTCATTCGGCAATCGTGATGAAGCAAGT	970
Db	917	TGGAGAGGCGCAGATGATGCTGCTGGAGCAGTCCGCCAACCGGACCCCGGCACT	976
Qy	971	TTGACAGACCGCACATGTTTGGATATCCCGCGC---CATCCCAATCGGCATATTCGGTTG	1027
Db	977	TCCCGGACCCGACACCTTCGACATCCCGCGCTCGAGCGCACCCCGGCATGGCTTCG	1036
Qy	1028	GCACGCGCATCCATTTTTCCTTGGGCGCCCGCTTGGCGCTCTTGAAGCAATATTCGGT	1087
Db	1037	GGCAGCGCATCCACCACTGCCTGGTGGTGGCGCTCGCCGCTCGAGGCGCAAGTTCATGC	1096
Qy	1088	T 1088	
Db	1097	T 1097	
RESULT 8			
US-10-680-860A-1			
; Sequence 1, Application US/10680860A			
; Publication No. US20050202528A1			
; GENERAL INFORMATION:			
; APPLICANT: BLONDELET-ROUAULT, Marie-Helene			
; APPLICANT: DOMINGUEZ, Helene			
; APPLICANT: DARBON-RONGERE, Emmanuelle			
; APPLICANT: GERBAUD, Claude			
; APPLICANT: GONDRAN, Anne			
; APPLICANT: KARRAY, Fatma			
; APPLICANT: LACROIX, Patricia			
; APPLICANT: OESTREICHER-MERMET-BOUVIER, Nathalie			
; APPLICANT: PERNODET, Jean-Luc			
; APPLICANT: TUHILLE, Karine			
; TITLE OF INVENTION: POLYPEPTIDES INVOLVED IN THE BIOSYNTHESIS OF SPIRAMYCINS, NUCLEOT			
; FILE REFERENCE: FRV2002/0028 US NP			
; CURRENT APPLICATION NUMBER: US/10/680,860A			
; 2003-10-07			
; CURRENT FILING DATE: 2003-10-07			
; PRIOR APPLICATION NUMBER: FR 0212489			
; PRIOR FILING DATE: 2002-10-08			
; PRIOR APPLICATION NUMBER: FR 0302439			
; PRIOR FILING DATE: 2003-02-27			
; PRIOR APPLICATION NUMBER: US 60/493,490			
; PRIOR FILING DATE: 2003-08-07			
; NUMBER OF SEQ ID NOS: 161			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 1			
; LENGTH: 30943			
; TYPE: DNA			
; ORGANISM: Streptomyces ambofaciens			
US-10-680-860A-1			
Query Match 11.0%; Score 130.6; DB 22; Length 30943;			
Best Local Similarity 48.0%; Pred.No. 2.7e-29;			
Matches 404; Conservative 0; Mismatches 434; Indels 3; Gaps 1;			
Qy	251	TGGACCCGCGGAGCATACAAATTCGTTTCAGTTCGTGAACAAAGCTTTACTTCGCGCGG	310
Db	914	TGGACCCGCGGAGCATACAAATTCGTTTCAGTTCGTGAACAAAGCTTTACTTCGCGCGG	973
Qy	311	TGATGAGCAATGGGAGCGAGATTCAGAAATTCAGATGATGATTCAAAATTC	370

RESULT 9
US-10-229-148B-1/c
; Sequence 1, Application US/10229148B
; Publication No. US20040091975A1
; GENERAL INFORMATION:
; APPLICANT: Meiji Seika Kaisha, Ltd.
; TITLE OF INVENTION: Midecamycin biosynthetic genes
; FILE REFERENCE: 138451 US
; CURRENT APPLICATION NUMBER: US/10/229,148B
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 210516/2002
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 84428
; TYPE: DNA
; ORGANISM: Streptomyces mycarofaciens

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FEATURE:
NAME/KEY: CDS
LOCATION: Complement((1)..(675))
OTHER INFORMATION: ORF42 (fragment)
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((1168)..(2202))
OTHER INFORMATION: ORF41
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((2220)..(3215))
OTHER INFORMATION: ORF40
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((3237)..(4691))
OTHER INFORMATION: ORF39
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((4695)..(5948))
OTHER INFORMATION: ORF38
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((6048)..(6629))
OTHER INFORMATION: ORF37
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((6653)..(7945))
OTHER INFORMATION: ORF36
FEATURE:
NAME/KEY: CDS
LOCATION: (8149)..(9015)
OTHER INFORMATION: ORF35
FEATURE:
NAME/KEY: CDS
LOCATION: (9012)..(9335)
OTHER INFORMATION: ORF34
FEATURE:
NAME/KEY: CDS
LOCATION: (9328)..(10458)
OTHER INFORMATION: ORF33
FEATURE:
NAME/KEY: CDS
LOCATION: (10521)..(11603)
OTHER INFORMATION: ORF32
FEATURE:
NAME/KEY: CDS
LOCATION: (11729)..(12961)
OTHER INFORMATION: ORF31
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((13016)..(14044))
OTHER INFORMATION: ORF30
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((14074)..(15096))
OTHER INFORMATION: ORF29
FEATURE:
NAME/KEY: CDS
LOCATION: (15643)..(17466)
OTHER INFORMATION: ORF28
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((17522)..(18895))
OTHER INFORMATION: ORF27
FEATURE:
NAME/KEY: CDS
LOCATION: (19063)..(20229)
OTHER INFORMATION: ORF26
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((20307)..(21743))
OTHER INFORMATION: ORF25
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((21733)..(22527))
OTHER INFORMATION: ORF24
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((22534)..(23571))
OTHER INFORMATION: ORF23
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((23555)..(24463))
OTHER INFORMATION: ORF22
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((24460)..(25650))
OTHER INFORMATION: ORF21
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((25647)..(26105))
OTHER INFORMATION: ORF20
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((26180)..(27391))
OTHER INFORMATION: ORF19
FEATURE:
NAME/KEY: CDS
LOCATION: (27937)..(28983)
OTHER INFORMATION: ORF18
FEATURE:
NAME/KEY: CDS
LOCATION: (29244)..(42779)
OTHER INFORMATION: ORF1
FEATURE:
NAME/KEY: CDS
LOCATION: (42823)..(48657)
OTHER INFORMATION: ORF2
FEATURE:
NAME/KEY: CDS
LOCATION: (48712)..(59802)
OTHER INFORMATION: ORF3
FEATURE:
NAME/KEY: CDS
LOCATION: (59850)..(64556)
OTHER INFORMATION: ORF4
FEATURE:
NAME/KEY: CDS
LOCATION: (64687)..(70365)
OTHER INFORMATION: ORF5
FEATURE:
NAME/KEY: CDS
LOCATION: (70365)..(71078)
OTHER INFORMATION: ORF6
FEATURE:
NAME/KEY: CDS
LOCATION: (71113)..(72360)
OTHER INFORMATION: ORF7
FEATURE:
NAME/KEY: CDS
LOCATION: (72400)..(73665)
OTHER INFORMATION: ORF8
FEATURE:
NAME/KEY: CDS
LOCATION: (73694)..(75043)
OTHER INFORMATION: ORF9
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((75899)..(76570))
OTHER INFORMATION: ORF10
FEATURE:
NAME/KEY: CDS
LOCATION: Complement((76602)..(77765))
OTHER INFORMATION: ORF11
FEATURE:
NAME/KEY: CDS
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; LOCATION: (78039)..(79313)
; OTHER INFORMATION: ORF12
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((79391)..(81052))
; OTHER INFORMATION: ORF13
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (81541)..(82356)
; OTHER INFORMATION: ORF14
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82760)..(83362)
; OTHER INFORMATION: ORF15
; FEATURE:
; NAME/KEY: CDS
; LOCATION: Complement((83495)..(84142))
; OTHER INFORMATION: ORF16
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (84329)..(84428)
; OTHER INFORMATION: ORF17 (fragment)
US-10-229-148B-1

Query Match      10.2%; Score 121; DB 18; Length 84428;
Best Local Similarity 47.2%; Pred. No. 6e-26;
Matches 401; Conservative 0; Mismatches 445; Indels 3; Gaps 1;

QY 239 CCATCATTTAAGTACCGCCGCGAGCATACAAAATCGTTCACTGTGAACAAGCCT 298
    |||||
DB 27147 CCATCGCGCCCTCGACCGCCGCGCCGCGGCGGCGGCGGCGGCGGCGGCGG 27088

QY 299 TTACTCCGCGGTGATGAAGCAATGGGAACCGAGAAATTCAGAAATTCACAGATGAAC 358
    |||||
DB 27087 TCACCCCGCGGATGGCCGCTTGGAAACCCCGCATCGGCCGCTCACTCGAGAGTCC 27028

QY 359 TTCAAAAATTTCCAGGGGCGCAGTGTGACCTTTGTTACAGATTTTTCATACCCGCTTC 418
    |||||
DB 27027 TCGATCGGTGCGCGCCGAGGAGACCATCGACGTGCTGGCGACCTCTCTACGCGCTGC 26968

QY 419 CGGTTATTGTGATATCTGAGCTGCTGGAGTGCTCTTCAGCGCAGATGGAACAGTTTAAG 478
    |||||
DB 26967 CGGTATCGTATCGCCGAGCTGCTGGGCATACCGTCCGGTACCGCGATGTGTTCCGCG 26908

QY 479 CATGCTCTGATCTTCTGGTTCAGTACACCGAAGGATAAAGTCAAGAAGCTGAAAAAGCCT 538
    |||||
DB 26907 GGTGGGTGACACCTGTCTCACCAGAGGGGCTGGAGTACCCGAACTCCCGGACACT 26848

QY 539 TTTTGGAAAGACGAGATAAGTGTGAGGAAGAACTGGCCGCGTTTTTTGCCGCGCATATAG 598
    |||||
DB 26847 TCAGCGAGACGATCGCCCGCCGCTCAAGGAGATGACCGACTATCTCTGACACGATCC 26788

QY 599 AGAAAGGGAACAAACCGGAACAGGATATTTTCTATTTTAGTGAAGCGGAAGAA 658
    |||||
DB 26787 AGCCAAGCGGAGGCGCGGCTGCGACGACCTGATCAGCGGCTGTGTCAGGCGGAGCAGG 26728

QY 659 CAGGCGAGAAGCTGTCCGGTGAAGAGCTGATTCCGTTTTTGACGCTGCTGTGGTGGCG 718
    |||||
DB 26727 AGCGCGCAGAGCTACCGACGCTGGAGATCGTCAACATCGTGCCCTGTCTCACCAGCG 26668

QY 719 GAAATGAACCACTACAACTGTATTTCAATGCGATGTPACAGCATATTTAGAAACGCCAG 778
    |||||
DB 26667 GCCAGTCTCGTCAAGACGCTGCTCAGCAACCTCTCTCTGTTCTGGAGGAGAACCCGC 26608

QY 779 GGGTTTACGAGAACTGGCGACCCATCTGAACTGATGCTCAGCGATGAGGAGGCT 838
    |||||
DB 26607 AGGCGCTGCGGACCTGCGCGCGGACCGCGAGCTGGTACCGGCTGCGGTGGAGGAGACAC 26548

QY 839 TCGGTTTACAGAGCGCGCGCCCGGTTTTTGAGGCGCATTTGCCAAGCGGATACGGAGATCG 898
    |||||
DB 26547 TCGGCTACCGAGCGCCCTTCAACAACATCTTCGGTCTCTCAAGGAGGACACCGACATCC 26488

QY 899 GGGGGCACTGTATTAAGAAAGGTGATATGGTTTTGGCGTTTTGTGGCATCGGCAATCGTG 958
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Db 26487 TCGGCCCGGAAATGAAGAAGGCGCAGATGGTTCATCGCTGGAGCAGTCGCGCCAAACCGCG 26428
QY 959 ATGAAGCAAAAGTTTGACAGACCGGCACATGTTTGATATCCGCGGCATCCCA--ATCCGC 1015
Db 26427 ACCCGAACACTTCCCGGAGCCCGACACCTTCGACATCCGACGCTCAAGCAGCTCCCGCC 26368
QY 1016 ATATTGGGTTGGCCAGGCGATCCATTTTTCCTTTGGGGCCCGCTTGCCTGCTTTGAAG 1075
Db 26367 ACATGGGCTCGGCATCGGTATTCCACCACTGCCCTGGGGCCCTTCTGGCACGTCAAGGAAG 26308
QY 1076 CAAATATCG 1084
Db 26307 GCAAGGTGG 26299

RESULT 10
US-10-214-446-39
; Sequence 39, Application US/10214446
; Publication No. US20030180742A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David
; APPLICANT: Burk, Mark J.
; APPLICANT: Hitchman, Tim
; APPLICANT: Pujol, Catherine
; APPLICANT: Richardson, Toby
; APPLICANT: Short, Jay M.
; TITLE OF INVENTION: P450 ENZYMES, NUCLEIC ACIDS ENCODING
; TITLE OF INVENTION: THEM AND METHODS OF MAKING AND USING THEM
; FILE REFERENCE: 09010-500001
; CURRENT APPLICATION NUMBER: US/10/214,446
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 60/309,497
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Bacterial
US-10-214-446-39

Query Match      10.1%; Score 120.4; DB 16; Length 1215;
Best Local Similarity 49.6%; Pred. No. 6.1e-27;
Matches 418; Conservative 0; Mismatches 391; Indels 33; Gaps 3;

QY 241 ATCATTAACATGGACCGCCCGACAGCATACAAAATTCGTTCACTGTAACAAGCCCTTT 300
    |||||
DB 277 ATCCTCAGCATGGACCGCCCGGACCAACACCGGTTGGCGACCCCTGGTGGCCAAAGCGTTC 336

QY 301 ACTCGGCGGTGATGAAGCAATGGAAACCGAGAAATTCAGAGAAATCACAGATGAACCTGATT 360
    |||||
DB 337 ACCATGACCAAGTGGAGAGTTGCGCCGCGGTGGGAGCTGGCCGACGAGCTGATC 396

QY 361 CAAAAATTTACGGGGCGCAGTGA---GTTTGACCTTGTTCACGATTTTTCATACCCGCTT 417
    |||||
DB 397 GACAAGATGGTCGCCACCGCGCCCGCTCGACTGGTCGAGGAGTTTCGCTGCGCGTG 456

QY 418 CCGGTTATTGATATCTGAGCTGCTGGAGTGCCTTTCAGGCGAGATGGAACAGTTTAAA 477
    |||||
DB 457 CCGTTCGGGGTGTCTGCCAGCTGCTCGGCGTGCCTGCGAGGACCGTCCCGGCTTCGG 516

QY 478 GCATGGTCTGATCTTCTGGTCACTACACCGAAGGATAAAAGTGAAGAGCTGAAAAAGCC 537
    |||||
DB 517 GCGTGGAGCGCGCGGCTGTCCACCAGTTCCCTGACCGCGGAGAGTTTCGACGCCAAC 576

QY 538 TTTTGGAAAGAACGAGATAAGTGTGAGAAAGAACTGGCCGCGGTTTTTTTTCGCGGATCAT 597
    |||||
DB 577 C-----AGGAGAACTGGCGGCTTACATCGCGGGGTTGATC 612

QY 598 GAAGAAAGCAACAAACCGAACAGGATATTTCTATTATTTAGTGGAGCGGAAGAA 657
    |||||
DB 613 GAGGATACCCGGGCGGTCCCGGTGAGGACCTGATCACCGGCTGATCGAGGCCCGGAC 672
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; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match          9.9%; Score 117.8; DB 15; Length 9025608;
Best Local Similarity 47.9%; Pred. No. 1.3e-23;
Matches 406; Conservative 0; Mismatches 432; Indels 9; Gaps 2;

QY 245 TTAACATGACCGCGCGAAGCATACAAAATCCGTTTCAGTCGTGAACAAAGCCTTTACTC 304
Db 2902578 TGACCAAGGACGCGCCGACACACGCGGCTGCGTGGCTCTCGACCGCTTCACGG 2902519

QY 305 CCGCGGTGATGAAGCAATGGGAACCGAGAAITTCAGAAATCACAGATGAATGATTCAAA 364
Db 2902518 CCGCGCGGTGCGAGGCGCTGCGCGCACAGGTGCAGACATCACGACGCGGCTCTCTCGACA 2902459

QY 365 AATTTTCAGGGCGCAGTGATGTTGACCTTGTTCAGATTTTTCATACCGCTTCCGGTTA 424
Db 2902458 CGATCGTCCCCCGGGCAGGCGGAGCTGATCGGCGACTTCGCTTCCGCTGGCGATCA 2902399

QY 425 TTGTGATATCTGAGCTGCTGGGAGTGCCCTTCAGCGCAGATGGAACAGATTTTAAAGCATGT 484
Db 2902398 CGGTGATCTGTGAACTGTCTGGGAGTGCCCAAGCGGACGAGACGTGTTCCGCCAGTGA 2902339

QY 485 CTGATCTTCTGTGTAGTACACCGAAGGATAAAAGTGAAGAGCTGAAAGCCTTTTGG 544
Db 2902338 CGAA-----GGACTTCCGCGGTGGACGAAACACCGACTCCCGCCAGCGCGCGGTG 2902285

QY 545 AAGAACGAGATAAGTGTGAGGAAGAACTGCGCGCGTTTTCGCGGCATCATAGAAGAA 604
Db 2902284 AGCGCGCGCGGTGCGAGCTGCGCGACCTCTCGAATATCTGACCGCATGTTGCAACAGC 2902225

QY 605 ACGGAAACAAACCGGAACAGGATATTTATTTCTATTTAGTGAAGCGGAAGAAACAGGCG 664
Db 2902224 GCGGTGAGGACCGCGCGACGAGCTGTTGACGCGCTGATCGCGCGCGGACGACGAGC 2902165

QY 665 AGAAGCTGTCCGGTGAAGAGCTGATTCGGTTTTTGACGCTGTCTGTGTGGCGCGGAATG 724
Db 2902164 ACCGGCTGAACGAGGCGGAGTTGCTGTCCATGATGTCTGCTGTCTGCTGCGCGCTTCG 2902105

QY 725 AAACCACTACAAACCTGATTTCAAATGCGATGTACAGCATATTAGAAGCCGACGCGTTT 784
Db 2902104 AGACGACGCTCAATCTGATCGGCAACGCGACCCCTGGCCCTGCTGGCCACCCCGACCAAC 2902045

QY 785 ACGAGGAATCGGCGAGCCATCTGAACTGATGCTCAGGCACTGGAGGAAGCTTTCGCTT 844
Db 2902044 TCGCCCTGTGCGCGAGCCACCGAACTGTGTGACTCGCGCTGGAGGATGCTGCGGT 2901985

QY 845 TCAGAGCGCGCGCGCGGTTTTGAGCGCATTTGCCAAGCGGATAGC---GAGATCGGG 901
Db 2901984 ACGACGGGTGTTTCGAGACGCGGACGTGGCGGTTCCCGCTCGAACCCTATCGAGGTGGCGG 2901925

QY 902 GGCACCTGATTAAGAAGTGATATGTTTTGCGGTTTGTGTCATCGGCAAAATCGTGATG 961
Db 2901924 GCACGGCATCGAAGAGGCGCACCCGGTGCTCTGTCTCCCTGGCATCGGCAACCGGAGC 2901865

QY 962 AAGCAAAGTTTGAACAGACCGCATGTTTGTATATCGCGCCCATCCCAATCGCGATATTG 1021
Db 2901864 GGGCGAAGTTCCCGGACCGGACGACTTCGACGTACACCGCGCGGACCCCGCCACGTG 2901805

QY 1022 CGTTTGGCCACGCGATCCATTTTTTGGCTTTGGGGCCCGCGTTCGCGCTTTTGAAGCAATA 1081
Db 2901804 CCTTGGGCGGGGTGCGCATTTCTGCTCTGGTGTCTCCCTGCGCGGCTGGAGGGCCGGA 2901745
```

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QY 1082 TCGCGTT 1088
Db 2901744 TCGCGTT 2901738

RESULT 13
US-10-156-761-4523
; Sequence 4523, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 4523
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1215)
US-10-156-761-4523
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Query Match          9.7%; Score 115.4; DB 15; Length 1215;
Best Local Similarity 47.9%; Pred. No. 2.4e-25;
Matches 402; Conservative 0; Mismatches 426; Indels 11; Gaps 2;

QY 236 ATTCATCATTTAATGATGAGCCCGCGAAGCATACAAAATCCGTTTCAGTCGTGAACAAAG 295
Db 269 ATGGGATGCTCGACTCGAGCGCGCGGACCAACCCCGATCAGGCGCTGCTGTGCGAAGG 328

QY 296 CTTTACTTCCGCGCTGATGAAGCAATGGGAACCGAGAAITTCAGAAATCACAGATGAAC 355
Db 329 CGTTACCGCGCGACCGGTGAGCAGCTCAAGCGTACGTGGCCCAAGCTCGCCGCGAGC 388

QY 356 TGATTTAAAAATTTTCAGGGCGCAGTGAAGTTGACCTTGTTCACGATTTTTCATACCGCG 415
Db 389 TGGTGGACCGGCTCGTCCGCGCGCGCGGGGATCTGCTCGCGATGTCGCCGAGCGCC 448

QY 416 TTCGGTTATTGTATATCTGAGCTGCTGGAGTGCCCTTCAGCGCAGATGGAACAGTTTA 475
Db 449 TCCCGGTGGCGCTCATCGCGAGATGCTGGGCACTCCCGAGTCCGACCGCTGCCCGCTCC 508

QY 476 AAGCATGCTGTGATCTTCTGTGATGACACCGAAGGATAAAAGTGAAGAGCTGAAAAAG 535
Db 509 GTCCCTGTGCG-----CGACATCTGCGGATGTACAGAGCTGAACCCCGCGAAG 558

QY 536 CTTTTTGGAAAGACGAGATAAGTTG-AGGAAGAACTGGCGCGGTTTTTTCGCGGCATC 594
Db 559 GACGTGGCGGGAAGGCGGTGCGGCGTCTCGGATCTCCGACTACCTCGCGAGCGCTG 618

QY 595 ATAGAGAAAGCGAACAACCCGAAACAGAGATATTCTTCTATTATTAGTCGAGCGGAA 654
Db 619 ATCCCGAGCGCCCAAGGAGCCCGGCGACGATCTCATCTCGGGGCTCATCGCGCCCAT 678

QY 655 GAAACAGCGGAGAGCTGCTCCGCTGAAGAGCTGATTCGTTTTTGACCGCTCTGCTGTG 714
Db 679 GACGAGCGGAGCGCTCACCAGCAGAGAGATGATCTCCACCTGGTCTGCTGCTCAAC 738

QY 715 GCCGAAATGAACCACTACAAACCTGATTTCAAATGCGATGTACAGCATATTAGAAACG 774
```

Db 739 GCGGCCACGAGGCCACCGTCAACGCCACGGTCAACGGCTGTGTACGCTTGTTCGCAAC 798
Qy 775 CCAGCGCTTACGAGAACTCGGAGCCATCTCTGAACCTGATGCTCTCAGGACAGTGGAGAA 834
Db 799 CCGGACAGCTGGCGCCCTGGGCGCCACACTCGTCTGTGCGCGCGCTGGAGAG 858
Qy 835 GCCTTGCCTTTACAGAGCGCGCGCGCTTTTGAAGCGCATTTGCCAAGCGCGATACGAG 894
Db 859 TTGATGCGCTACGACACGCCCTCTCAGCTCTTCGAGCGCTGGTCTTGAGAGATCGAG 918
Qy 895 ATCGGGGGACCTGATTAAGAGGTGATATGTTTGGGCTTGTGGCATCGGCAAT 954
Db 919 ATCGAGCGCAACGAGGTCCGAGGGCGCGAGATCGCCATGCTTTTGGCTCCGCGCAAC 978
Qy 955 CGTGATGAAGCAAAAGTTTGACAGACCGCACATGTTTGATATCCGCGCCATCCCAATCCG 1014
Db 979 CACGACCCGAGGTCTTCGGAATCCCGAGAACTCGACCTCACCGGGAGGACACCCC 1038
Qy 1015 CATATTGCGTTTGGCCACGGCATCCATTTTTCCTTGGGGCCCCGCTTGGCCGCTTTGA 1073
Db 1039 CACATTTCTTACGGCGGGCATCCACTACTGCTATCGGGGACCGCTGGCACGGATCGA 1097

RESULT 14

US-10-156-761-6226
; Sequence 6226, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6226
; LENGTH: 1164
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1164)
US-10-156-761-6226

Query Match 9.6%; Score 114.2; DB 15; Length 1164;
Best Local Similarity 48.2%; Pred. No. 5.7e-25;
Matches 409; Conservative 0; Mismatches 413; Indels 27; Gaps 2;
Qy 240 CATCATTAACATGGACCGCGGACGATCAAAATCCGTTTCAGTCTGTGAACAAGCCTT 299
Db 231 CCTGCTCAACATGGACCGCGGACCAACCCGATCCGGCGCTGTGTCGGCGGCTT 290
Qy 300 TACTCCGCGCTGATGAAGCAATGGAAACCGAGAAATCAAGAAATCAAGATGAATCAT 359
Db 291 CACCTGTGCTCGCTCGAACAACTCCGCGAGCCCGTACGGAGACCGCCACCGCTTCT 350
Qy 360 TCAAAAATTCAGGGCGCAGTGTGACCTTGTTCACGATTTTTCATACCGCTTCC 419
Db 351 CGACGCACTCGGAGCGCACCGCAGCACCGACTCATCGCTCGTACGCGCGCCCTGCC 410
Qy 420 GGTATTGTGATATCTGAGCTGCTGGAGTGCCTTCAGCGCAGATGGACAGTTTAAAGC 479
Db 411 GATCACCGTCTATCTCGGACCTGCTCGCGTGTCCGAGCAACACCGCGGGGACTTCCGGGC 470

Qy 480 ATGCTCTGATCTTCTGTGTCTAGTACACCGAAGGATAAAAGTGAAGAGCTGAAAAAGCCTT 539
Db 471 CTGACCGACCGCTCTGTCTACCCCGGACCGCGCCCGCGAGCTGCGCAGGGAATCCGT 530
Qy 540 TTTGGAAGACGAGATAAGTGTGAGGAGAACTGGCGCGCTTTTTCGCGGCATCATA 599
Db 531 CGTCTCGT-----TGCTCGGCTTCTTCAACCGGCTCTCTCGC 566
Qy 600 AGAAAGCGAAACAAACCGGAAACAGGATATATTTCTATTTTATTTAGTGAAGCGGAAGAAC 659
Db 567 CGACAGCGCAAGAACCCCGCGGACGACCTGCTCTCGACCTCATCGCGTGCAGGAAGA 626
Qy 660 AGCGAGAACTGTCTGGTGAAGAGTGTATTCGTTTGTGACGCTGCTGTGTGTGGCGG 719
Db 627 GGGGACCGCTCACCGAGGACGAGCTGATGTCCTCGCTTCTCATCTCTTTCGCGCG 686
Qy 720 AATGAACCACTACAAACCTGATTTCAATGCGATGTACAGCATATTAGAAACGCCAGG 779
Db 687 CTACGAGAACCCGTGACCTCATCGGAAACGCGCTACTGGCGCTGCTGCGCCATCCGGA 746
Qy 780 CGTTTACGAGAACTGCGCAGCCATCTGAACTGATGCCTCAGGACGTGAGGAAAGCCTT 839
Db 747 GCAGCTCGCGCGCTCGCGAGGACCGCGCAGGCTCGCGACGCGCTCGGGAGTTGCG 806
Qy 840 GCGTTTCAGAGCGCGCGCCCGCTTT---TGAGCGCATTTGCCAAGCGGATACGAGAT 896
Db 807 CCGCTACGAAGGGCGCGCTGCTCGCATCCGCGCTTCCCGTGGCGGACGCTGACGAT 866
Qy 897 CGGGGGCAGCTGATTAAGAGTGTATGTTTGGCGTTTGTGCGATCGGCAATCG 956
Db 867 CGCGGGGTCAACCGTGGCGCGGGGAGACCGTGTCTGTGCTGTGTCGCGCGCAACCG 926
Qy 957 TGATGAAGCAAGTTTGACAGACCGCATGTTTGATATCCGCGCCATCCCAATCCGCA 1016
Db 927 TGACCGAGCGGTTTCCCGACCCCGACCGCTCGATCTGCGCGCGACGCGCGAGGCCA 986
Qy 1017 TATTGCGTTTGGCACCGCATCCATTTTTCCTTGGGGCCCCGCTTGGCGCTTTGAAGC 1076
Db 987 CCTCGCGCTCGGCACCGCGCTCCACTACTGCTGGGCGCGCGCTGCGCGGCTGGAGAC 1046
Qy 1077 AATATCGC 1085
Db 1047 GGAGTCCG 1055

RESULT 15

US-10-214-446-55
; Sequence 55, Application US/10214446
; Publication No. US20030180742A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, David
; APPLICANT: Burk, Mark J.
; APPLICANT: Hitchman, Tim
; APPLICANT: Fujol, Catherine
; APPLICANT: Richardson, Toby
; APPLICANT: Short, Jay M.
; TITLE OF INVENTION: P450 ENZYMES, NUCLEIC ACIDS ENCODING
; TITLE REFERENCE: THEM AND METHODS OF MAKING AND USING THEM
; FILE REFERENCE: 09010-500001
; CURRENT APPLICATION NUMBER: US/10/214,446
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 60/309,497
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Bacterial
US-10-214-446-55

Query Match 9.6%; Score 114.2; DB 16; Length 1248;

Best Local Similarity 46.7%; Pred. No. 6e-25;		Matches 399; Conservative 0; Mismatch 453; Indels 3; Gaps 1;	
Qy	230	TTGGAAATTCATCATTAACATGGACCGCCGCAAGCATACAAAATCCGTTCAAGTCGTGA	289
Db	263	TCGAGAACTGGCTCGTCTCTCTGGACCGCCCGCCGACACCGCGCTGCGCCAGGTGG	322
Qy	290	ACAAAGCCTTTTACTCGGCGGTGATGAAGCAATGGAAACCGAGAATTCAAGAAATCACAG	349
Db	323	CCCCCGCTGAGCGCTCGGCCGTACGGGCCCTTGGTCCCCCGCTACGGGAGATCGGG	382
Qy	350	ATGAATGTGATCAAAAATTTCAAGGGCGCAGTGAGTTTGACCTTGTTCACGATTTTTCAT	409
Db	383	AGGAATCTGTACGGCCCTCGCGCGCGCGCCGCTGCTCGAACTGTGTGAGGGCTTCGCG	442
Qy	410	ACCCGCTTCCGTTATTTGTGATATCTGAGCTCTGGAGTGCCCTTCAGCGCAGATGGAAC	469
Db	443	CCCCGTCCCGCTGCTGTGCTGTGGCGGGCTGCTCGGGGTGACCCCGCTCGGTGGCCGT	502
Qy	470	AGTTTAAAGCATGGTCTGATCTTCTGGTCAGTACACCGAAGGATAAAAGTGAAGAAGCTG	529
Db	503	GGTTCGGGAGAGGGG---CTCGCCCTCCAGCGGTCCGGCGGGACCGGGCGACCGGT	559
Qy	530	AAAAAGCCTTTTGAAGAACGAGATAAGTGTGAGGAAGAACTGGCCGCGTTTTTTGCGG	589
Db	560	CGCGCGCGCGCTCGCACGGGCGGACCGCGCGCGCGCACCTTGACGCGTACTTCCGGG	619
Qy	590	GCATCATAGNAGAAAGCAAAACCGGAACAGGATATTTATTTAGTGGAG	649
Db	620	CGGAGCTGGCGCGCGCGCTCGGAGGACCGGGGGACCTGCTCTCGGCGTGGCGCGG	679
Qy	650	CGGAAGAAACAGCGGAGAGCTGTCCGGTGAAGAGCTGATTCGGTTTTGACGCTGCTGC	709
Db	680	CGGGCGCGAGACCCCTCGCTGGGGACGACCGCGCTGACGTGACCTGCGTCCACCTCC	739
Qy	710	TGGTGGCGGAATGAACCACTACAAACCTGATTTCAAAATCGGATGTACAGCATATTAG	769
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Qy	770	AAACCCAGCGCTTTACGAGGAACCTGCGAGCCATCCTGAACCTGATGCTCAGGCAGTGG	829
Db	800	CGCGCGCGGAGTGGCGGAGAACTGCGCGCGGACCCGGGCGCTGTGCGGAACGCGGTGG	859
Qy	830	AGGAAGCCTTGGCTTTCAGAGCGCGCCCGCTTTGAGGCGCATTGCCAGCGGGATA	889
Db	860	ACGAGTCTCTGCCACGACCCACCCGCTGCAGATGGTACGCGGTGGGCGCGCGGACG	919
Qy	890	CGGAGATCGGGGGCACCTGATTAAAGAGGTGATATGGTTTTTGGCGTTTGTGGCATCGG	949
Db	920	CGGAGCTCGCCGCGGAGCGGTCCGCGGGGCGACCGGGTCCAGCTGGTGTGGGTTCGG	979
Qy	950	CAAATCGTGATAGCAAAAGTTTGACAGACCGCATGTTTGATATCCGCGCCATCCCA	1009
Db	980	CCCACCGCACCGGCGCGCTTCCCGGACCCCGACCGGCTGGACATCCGCGCGGACCG	1039
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Db	1040	GCCGGCACTGCGGTTCTGGGATCCACTACTGCTGGGGGGCGGCTGGCACGG	1099
Qy	1070	TTGAAGCAAAATCG	1084
Db	1100	CGGAGCGGAGATCG	1114

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Job time : 1016 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 11:04:58 ; Search time 238 Seconds
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Title: US-09-869-334B-2

Perfect score: 1191

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	139.2	11.7	8478	3	US-08-676-818-1
2	139.2	11.7	8478	3	US-09-407-549-1
C 3	118.2	9.9	4403765	3	US-09-103-840A-2
C 4	118.2	9.9	4411529	3	US-09-103-840A-1
5	116.4	9.8	4403765	3	US-09-103-840A-2
6	116.4	9.8	4411529	3	US-09-103-840A-1
7	111.4	9.4	1194	3	US-08-765-907A-9
8	111.4	9.4	1194	4	US-09-987-614A-9
9	111.4	9.4	4496	3	US-08-765-907A-6
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14	103.6	8.7	6085	3	US-09-029-603-4
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18	88.8	7.5	1233	4	US-09-266-965-24
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20	88.8	7.5	18331	4	US-09-266-965-96
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23	85.8	7.2	1221	6	5212296-16
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25	85.8	7.2	1879	6	5212296-5
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30	84.4	7.1	1227	4	US-09-385-040-23
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C 44	80.4	6.8	47981	4	US-09-679-279-1
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ALIGNMENTS

RESULT 1

US-08-676-818-1
; Sequence 1, Application US/08676818
; Patent No. 6057136
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley Grant
; APPLICANT: Perkins, John B.
; APPLICANT: Vocum, R. Rogers
; APPLICANT: Pero, Janice G.
; TITLE OF INVENTION: BIOTIN BIOSYNTHESIS IN BACILLUS
; TITLE OF INVENTION: SUBTILIS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/676,818
; FILING DATE: 08-JUL-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/239,430
; FILING DATE: May 6, 1994
; APPLICATION NUMBER: 08/084,709
; FILING DATE: June 25, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 04599/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8478
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-676-818-1

Query Match 11.7%; Score 139.2; DB 3; Length 8478;

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Best Local Similarity 50.4%; Pred. No. 2.7e-36; Mismatches 408; Indels 12; Gaps 3;
Matches 426; Conservative 0;

QY 252 GACCCGCGGAGCATACAAAATCGGTTCAGTGTGAAACAAAGCCTTTACTCCGCGGT 311
Db 5735 GAACAGCCTGATATAGACGATTCGGGACGCTTCCAGCGGAGCGTTTACCGGAGAAC 5794
QY 312 GATGAAGCAATGGGAAACCGAGAAATTCAGAAATACAGATGAATCAAAAATTTCA 371
Db 5795 GACAGAGTTATACGCCGTATATCATTTGAAACTGTCCATCTTTGTTGATCAAGTGA 5854
QY 372 GGGGCGCAGTGTGACCTTTGTCACGATTTTTCATACCGCTTCGCGTTTATGTGAT 431
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QY 432 ATCTGAGCTGTGGGAGTGCCTTCAGCGCAGATGGAACAGTTTAAAGCATGTCTGATCT 491
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QY 492 TCTGGTCAGTACACCGAAGGATATAAGTGAAGAGCTGAAAGCCTTTTGGAAAGACG 551
Db 5975 TCTCAT-----TCNAACGATTTATTTACCGCTCAAGAAAGGATTAACAGAGGCA 6027
QY 552 AGATAAGTGTGAGGAAGAACTCGCCGCGTCTTTTCCCGCATCATAGAGAAAGCGAAA 611
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QY 672 GTCCGGTGAAGAGCTGATTTCCGTTTTCACGCTGTCTGTGGCGGAAATGAACACAC 731
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QY 732 TACAACCTGATTTCAAATGCGATGTACAGCATATTTAGAAACGCGAGCGTTTACAGGA 791
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RESULT 2
US-09-407-549-1
; Sequence 1, Application US/09407549
; Patent No. 6303377
; GENERAL INFORMATION:
; APPLICANT: Bower, Stanley Grant
; APPLICANT: Perkins, John B.
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Pero, Janice G.

```
; TITLE OF INVENTION: BIOTIN BIOSYNTHESIS IN BACILLUS  
; TITLE OF INVENTION: SUBTILIS  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/407,549  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/239,430  
; FILING DATE: May 6, 1994  
; APPLICATION NUMBER: 08/084,709  
; FILING DATE: June 25, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Freeman, John W.  
; REGISTRATION NUMBER: 29,066  
; REFERENCE/DOCKET NUMBER: 04599/004001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8478  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-09-407-549-1
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Query Match 11.7%; Score 139.2; DB 3; Length 8478;  
Best Local Similarity 50.4%; Pred. No. 2.7e-36;  
Matches 426; Conservative 0; Mismatches 408; Indels 12; Gaps 3;  
  
QY 252 GACCCGCGGAGCATACAAAATCGGTTCAGTGTGAAACAAAGCCTTTACTCCGCGGT 311  
Db 5735 GAACAGCCTGATATAGACGATTCGGGACGCTTCCAGCGGAGCGTTTACCGGAGAAC 5794  
QY 312 GATGAAGCAATGGGAAACCGAGAAATTCAGAAATACAGATGAATCAAAAATTTCA 371  
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Db 5855 AGGTAAAAAAGATGGAGTCAATTCGGGACTTGTCTTCTTTAGCAAGTTTGTGAT 5914  
QY 432 ATCTGAGCTGTGGGAGTGCCTTCAGCGCAGATGGAACAGTTTAAAGCATGTCTGATCT 491  
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QY 492 TCTGGTCAGTACACCGAAGGATATAAGTGAAGAGCTGAAAGCCTTTTGGAAAGACG 551  
Db 5975 TCTCAT-----TCNAACGATTTGATTTTACCGCTCAAGAAAGCAATTAACAGAGGCA 6027  
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Db 6203 GGTCAATCTCATCAGCAATTCAGTCCCTTGTCTGCTGCGCATCCAGAACAGCTTTGAA 6262
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RESULT 3

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US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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Query Match 9.9%; Score 118.2; DB 3; Length 4403765;
Best Local Similarity 48.1%; Pred. No. 5.1e-27;
Matches 401; Conservative 0; Mismatches 423; Indels 9; Gaps 2;

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Db 3948025 ATGATCGACATGGAGATCCCGCATCTGTTGGCGCGCAAGCTGTTAAACGCGGCTTC 3947966
Qy 301 ACTCGCGCGGTGATGAAGCAATGGAAACCGAGAAATTCAGAGAAATCACAGATGAATGATTT 360
Db 3947965 ACCGCAAGCGGTGATGAAGCAAGAGGCGTCGATTGCGCGCTGTGTGACACCCCTGATC 3947906
Qy 361 CAAAAATTCAGGGCGGAGTGGATTTGACCTTGTTCAGGATTTTCATACCCCGCTTCG 420
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Qy 661 GCGGAGAAGCTGTCCGCTGAAGAGCTGATTCGCTTTTTCACGCTGCTGCTGGCGCGGA 720
Db 3947614 GCGGAGCGCTAAGCGACGACGAGCTGCTCATGAGACGCTGCTGATCCCTGATCGCGGC 3947555
Qy 721 AATGAACCACTACAAACCTGATTTCAAATGCGATGTACAGCATATTAGAAACGCCAGGC 780
Db 3947554 GACGAGACCAACCGGCATACCTTGAGCGTGGTACCGAGCAGCTGCTCGCAACCGTAC 3947495
Qy 781 GTTTACGAGGAACCTGCGCAGCCATCTGAACTGATGCTCAGGACGATGGAAGGAAAGCCTTG 840
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Qy 901 GGCACCTGATTAAGAAAGTGATATGTTTGGCGTTCGTCGTCGTCGTCGCAAAATCGTGAT 960
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Qy 961 GAAGCAAAAGTTTGACAGACCGCACATGTTTGTATATCCGCGCCATCCCAATCCGCATATT 1020
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Qy 1021 GCGTTGGCCACGCGATCCATTTTGCCTTGGGCGCCCGCTTGCCTCTTGA 1073
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RESULT 4

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US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Query Match 9.9%; Score 118.2; DB 3; Length 4411529;
Best Local Similarity 48.1%; Pred. No. 5.1e-27;
Matches 401; Conservative 0; Mismatches 423; Indels 9; Gaps 2;
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QY 241 ATCATTAATGAGCCGCGGAGCATACAAAATCCGTTTCAGTCGTGAAACAAAGCCTTT 300
Db 3955295 ATGATCGACATGACGATCCCGCACATCTGTTGCGCGCAAGCTGTTAAACGCGGCTTC 3955236
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Db 3955235 ACCCGCAAGCGGTTGAAGACAAAGAGGCGTGCATTTGCGCGCTGTGTGACACACCTGTATC 3955176
QY 361 CAAAAAATTCAGGGCGGAGTCAGTTTGCACCTTGTTCACGATTTTTCATACCCGCTTCGG 420
Db 3955175 GACGCGGTGTGGAACCGCGCGAGTGTGACTTCTGTGCGGAGCCTGGCGCGCGCTACCG 3955116
QY 421 GTTATTGTGATATCTCAGCTGCTGGGAGTGCCTTCAGCGCAGATGGAACAGTTTAAAGCA 480
Db 3955115 ATGGCGGTGATCGCGGACATGCTCGGGTGCCTCCAGAGCAGCGGACATGTTCTTCGGG 3955056
QY 481 TGGTCTGATCTTCTGGTCAATGACCGAAGGATTAAGTGAAGAGCTGAAAAAGCCTTTT 540
Db 3955055 TGGTCCGACGATCTGGTGA-CATTCTCAGTTTCGATGTGTCTCAAGAGGATTTCCAGAT 3954997
QY 541 TTGGAAGAACGAGATAAGTGTGAGGAAGAACTGGCGCGTTTTTCGCGGCATCATAGAA 600
Db 3954996 CACCATGAGCGCTTCGCGGCGCTCAACGACTTCAACCGG-----GCCACCATTCGG 3954945
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Db 3954944 GCACGCGAGCGGACCCACACGACCTGGTCAGCGTGTCTGGTGAATTCGAAAGTTGAC 3954885
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QY 721 AATGAAACCACTACAAACCTGATTTCAAATGCGATGTACAGCATATTAGAAACGCGAGC 780
Db 3954824 GACGAGACACCGCGGATACCTTGAGCGGTGTATCCGAGAGCTGCTGCGCAACCGTGAC 3954765
QY 781 GTTTACGAGGAACCTGCGAGCCATCTCGAACTGATGCTCTCAGGCGAGTGAGGAAGCCTTG 840
Db 3954764 CAGTGGGACCTGCTGACGCGCACCGCTGCTGCTGCGCGGCGCATCGAGGAGTGCTA 3954705
QY 841 CGTTTCAGAGCGCGCGCGCGCTTTTGGCGCATTTGAGCGCATTTGCAAGCGGATACGGAGATCGGG 900
Db 3954704 CGTTGGACCGCGCCCGGTAAAGAACATGTGCGGGGTGTTGACCGCGGATACCGAGTTTCAC 3954645
QY 901 GCGCACCTGATTAAGAGAGTGCATATGTTTTGGCGTTTGTGGCATCGCAAATCGTGAT 960
Db 3954644 GGCACGGCTGTGTGTCGCGCGAGAGATGATGCTGCTCTTCGATGCGCGAACTTCGAC 3954585
QY 961 GAAGCAAAAGTTTGACAGACCGCACATGTTTGATATCCGCGGCATCCCAATCCGCATATT 1020
Db 3954584 GAGCGGTTTTCTGTGMAACCGGAAAGTTTGTATGTTTCAGCGAAATCCAAACAGCCACTTG 3954525
QY 1021 GCGTTTGGCAGCGGATCAATTTTTCCTTTGGGGCGCGCTTGGCGGCTTTGA 1073
Db 3954524 GCGTTTGGCTTCGCGACGCAATTTCTGCTGGGCAATCAGCTGCGCGGTTTGA 3954472
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RESULT 5

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US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
```

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; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 9.8%; Score 116.4; DB 3; Length 4403765;
Best Local Similarity 55.4%; Pred. No. 2.2e-26;
Matches 225; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 669 GCTGTCCGGTGAAGAGCTGATTCGGTTTTTGACCGCTGCTGCTGTGGCCGGAATGAAC 728
Db 874269 GCTGTCCGACGCCGAACCTGTACCTGTTCTTCATCTACTGTTACGCGCGCGCGGGAAC 874328
QY 729 CACTACAAACCTGATTTCAAATGCGATGTACAGCATATTAGAAACGCCAGCGGTTTACGA 788
Db 874329 CACCGTAACTCCATTGCCGCGGCTGTGGCGTGGCCGAGAACCTGACCAACTGCA 874388
QY 789 GGAACCTGCGAGCATCTCTGAACTGATGCTCAGCAGCTGAGGAGAGCTTGGTTTCAG 848
Db 874389 AACGCTGCGAAGCGATTTTGAGTTGTTGCCGACTGCGATCGAAGAGATCGTGAGGTGGAC 874448
QY 849 AGCCCGCGCCCGGTTTGTAGCGCATTTGCCAGCGGATATCGGAGATCGGGGGGACCT 908
Db 874449 GTCGCGGTCACTGAAAGCGCGCACGGCTCCGCTGCGGTGAGCTTGGCGGCGCAGCC 874508
QY 909 GATTAAGAAAGGTGATATGTTTTGGCGTTTTGTGGCATTCGCAAAATCGTGATGAAGCAA 968
Db 874509 GATCAGCGCGGTGAGAAAGTTGTGTGGAGGGCTCGGCCAACCGTGATCCAGCGT 874568
QY 969 GTTTGACAGACCGCACATGTTTGATATCCGCGCGCATCCCAATCCGCATATTGGTTTGG 1028
Db 874569 GTTCGACCGCGGACGAGTTTCGATATCACCCGAAAAACCCAATCCGCACTGGGTTTCGG 874628
QY 1029 CCAGCGCATCCATTTTTCCTTTGGCGCCCGCTTGGCCGCTTGA 1074
Db 874629 TCAGGGGTGCATTAATGCTTGGCGGCAATCTGCTGCGGTGGAA 874674
```

RESULT 6

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US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Query Match 9.8%; Score 116.4; DB 3; Length 4411529;
Best Local Similarity 55.4%; Pred. No. 2.2e-26;
Matches 225; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 669 GCTGTCCGGTGAAGAGCTGATTCGGTTTTTGACCGCTGCTGCTGTGGCCGGAATGAAC 728
Db 872139 GCTGTCCGACGCCGAACCTGTACCTGTTCTTCCATCTACTGTTTCAGCGCGCGCGGGAAC 872198
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; ORGANISM: Streptomyces pristinaespiralis
US-09-987-614A-9

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Query Match          9.4%; Score 111.4; DB 4; Length 1194;
Best Local Similarity 48.5%; Pred. No. 2.7e-27;
Matches 415; Conservative 0; Mismatches 416; Indels 24; Gaps 3;

QY 249 CATGACCCGCGGAGCATACAAAATCCGTTTCAGTCGTGGAACAAAGCCTTTACTCCGCG 308
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
228 CATGACCCGCGGATGCACCGCACCTTGC CGCCCTGGTTCAGCAGGCTTACACCCCG 287
QY 309 COTGATGAAGCAATGGGAACCGAGAAATTCAGAAATCAGATGAACATGATTCAAAATT 368
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
288 CACCGTCGCGGACCTCGAACCGAGGTCAACCGAATGGCGCGCACTGCTCGACCGCGT 347
QY 369 TCAGGGGCGCAGTGATGCTTGTTCACCATTTTTCATACCGCTTCGCTTATGTT 428
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
348 CGACGGCGACA---CGTTCGACCTCGTTCGCCACTTCGCTACCGCTGCGCGTATCGT 404
QY 429 GATATCTGAGCTGCTGGGAGTGCCTTCAGCGCAGATGGAACAGTTTAAAGCATGCTCTGA 488
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
405 GATCGCGGAATCTCTCGGCTGCGCGCGCGCGCGACCGCACCTGTTCCGCTCTCTGTCCGA 464
QY 489 TCTTCTGTCAGTACACCG-----AAGGATAAAAGTGAAGAGCTGA 530
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
465 CCGGATGCTGCAGATGCAGGTGCGCGACCCGCGGACATGCAAGTTTCGGCGACGCGCGGA 524
QY 531 AAAAGCCTTTTGGGAAGACGAGATAAGTGTGAGNAGAACTGGCGCGCTTTTTCGCGG 590
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
525 CGAGGACTACCAACGCTCGTCAAGAACCCATGCGCGCATGCAAGCTTACCTCCACGA 584
QY 591 CATCATAGAAGAAAAGCGAAAACAAACCGGAACAGGATATTATTTCTATTAGTGAAGC 650
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
585 CCACGTACCGACCGCGCGCGCGCGCGCGCGCGGAAACGACCTGATCTCGACCTGTCGCGC 644
QY 651 GGAAGAAACAGCGGAGAGCTGTCGCGTGAAGAGCTGATTCGTTTGTGACGCTGCTGT 710
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
645 CCGCGTGGAGGGCGAACGACTCACCGACGAGCAGATCGTCGAATTCGGGGCGCTGCTGT 704
QY 711 GGTGCGCGGAATGAACCACTACAAACCTGAACCTGATGCTTCAATGCGATGTACAGCATATGA 770
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
705 GATGCGCGGCCACGCTCCACCTCACTGCTCGCGCAACACCGTGTGTCGCTGAAGGA 764
QY 771 AACGCGAGCGCTTACGAGGAACCTGCGAGCCATCTGAACTGATGCTCTCAGGCACTGA 830
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
765 CCACCCCGGGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCTGATCCCGCGCTGATCGA 824
QY 831 GGAAGCTTTGTTTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGATAC 890
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
825 AGAAGTACTGCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 884
QY 891 CGAGATCGGGGCGACCTGATTAAAGAGGTGATATGTTTGGCGTTTGTGCGCATCGCG 950
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
885 CTTCTTCGCGCGGACACCATCCCGCGCGGACGATGTCGTGTCCTCTCTCTGTCGCG 944
QY 951 AAATCGTGATGAAGCAAAAGTTTGAACAGACCGCACATGTTTGATATCCGCGCGCATCCCAA 1010
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
945 CAACACGACGAACAGGTCTTCACCGACCCCGACACCTCGACCTCGCGCGGAGGC-- 1002
QY 1011 TCCGCAATATGCGTTTGGCCACGGAATCCATTTTTCCTTTGGGCGCGCGCTTTCGCGCT 1070
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1003 -CGCCAGATCGCTTTCGGCGAGGATCCACTACTGCTGGCGCGCGCGCGCTGCGCGCGCT 1061
QY 1071 TGAAGCAAAATATCGC 1085
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1062 GGAGGGCGCGCATCGC 1076
```

RESULT 9

US-08-765-907A-6
; Sequence 6, Application US/08765907A
; Patent No. 6352839
; GENERAL INFORMATION:

```
; APPLICANT: BLANC, Veronique
; APPLICANT: THIBAUT, Denie
; APPLICANT: BAMA-JACQUES, Nathalie
; APPLICANT: BLANCHE, Francis
; APPLICANT: COUZET, Joel
; APPLICANT: BARRIERE, Jean-Claude
; APPLICANT: DEBUSSCHE, Laurent
; APPLICANT: FAMECHON, Alain
; APPLICANT: PARIS, Jean-Marc
; APPLICANT: DUTRUC-ROSSET, Gilles
; TITLE OF INVENTION: Streptogramins And Method For Preparing Same By
; TITLE OF INVENTION: Mutasynthesis
; FILE REFERENCE: Streptogramin genes
; CURRENT APPLICATION NUMBER: US/08/765,907A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 4496
; TYPE: DNA
; ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-6

Query Match          9.4%; Score 111.4; DB 3; Length 4496;
Best Local Similarity 48.5%; Pred. No. 7.1e-27;
Matches 415; Conservative 0; Mismatches 416; Indels 24; Gaps 3;

QY 249 CATGACCCGCGGAGCATACAAAATCCGTTTCAGTCGTGGAACAAAGCCTTTACTCCGCG 308
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2027 CATGACCCGCGGATGCACCGCACCTTGC CGCCCTGGTTCAGCAGGCTTACACCCCG 2086
QY 309 CGTGATGAAGCAATGGGAACCGGAATTCAGAAATCAGATGAACATGATTCAAAATT 368
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2087 CACGTGCGCGACCTCGAACCCACGCTCACGAACTGGCGGCACTGCTCGACGCGT 2146
QY 369 TCAGGGGCGCAGTGTGATTTGACCTTGTTCAGATTTTTCATACCGCTTCGCTTATGTT 428
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2147 CGACGGCGACA---CGTTCGACCTCGTCGCGCACTTCGCTTACCGCTGCGCGTATCGT 2203
QY 429 GATATCTGAGCTGCTGGAGTGCTTCAGCGCAGATGGAACAGTTTAAAGCATGCTCTGA 488
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2204 GATCGCGAACTCTTCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCTTTCGCTCTGTCGA 2263
QY 489 TCTTCTGTCAGTACACG-----AAGGATAAAAGTGAAGAGCTGA 530
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2264 CCGGATGCTGCAGATGCAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2323
QY 531 AAAAGCCTTTTGGGAAGAACGAGATAAGTGTGAGGAAGAACTGGCGCGGTTTTTTTTCGCG 590
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2324 CGAGGACTTACCAACGCTCTCGTCAAAGAACCCATCGCGGCCATGCAAGCTTACCTCCACGA 2383
QY 591 CATCATAGAAGAAAGCGMAACAAACCGGAACAGATATTATTTCTATTTTGTGGAAGC 650
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2384 CCAGTCAACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2443
QY 651 GGAAGAAACAGCGGAGAGCTGTCGCGTGAAGAGCTGATTCGTTTTCGACGCTGCTGCT 710
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2444 CCGGTGGAGGGCGAACGACTCACCGACGAGCAGATCGTCGAATTCGGGGCGCTGCTGCT 2503
QY 711 GGTGCGCGGAAATGAACCACTACAAACCTGATTTCAAATCGCATGTACAGCATATTAGA 770
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2504 GATGCGCGGCGACGCTCTCCACTCGCTCGGCAACACCGCTGCTGCTGCTGCTGAAGGA 2563
QY 771 AACGCCAGCGCTTTCAGGGAACCTGCGCAGCCATCTCACTGATGCTCAGGCGAGTGA 830
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2564 CCACCCCGGGCGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2623
QY 831 GGAAGCCTTTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 890
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2624 AGAAGTACTGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2683
QY 891 GGAGATCGGGGGCGACCTGATTAAGAGAGGTGATATGTTTTCGCGTTTGTGGCATCGCG 950
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 2684 CGTCTCCGCGCACCAACATCCCGCGGACGATGGTCTGTCCTCCCTGCTGTCGCG 2743
Qy 951 AAATCGTGATGAAGCAAAAGTTTGACAGACCCACATGTTTGATATCGCGCCCATCCAA 1010
Db 2744 CAACACAGCAACAGGTCCTTACCGACCCCGACCACTCGACCTCGCCCGGAGGC-- 2801
Qy 1011 TCCGATATTCGTTTGGCCACGGGATCCATTTTGGCTTGGGGCCCGCTTGGCCGCTCT 1070
Db 2802 -CGCAGATCCCTTGGCCACGGGATCCATCTGCTGGGCGCCCGCTCGCCGCT 2860
Qy 1071 TGAAGCAAAATATCGC 1085
Db 2861 GGAGGCCGCGATCGC 2875

RESULT 10

US-09-987-614A-6
; Sequence 6, Application US/09987614A
; Patent No. 683382
; GENERAL INFORMATION:
; APPLICANT: BLANC, Veronique
; APPLICANT: THIBAUT, Denis
; APPLICANT: BAMBAS-JACQUES, Nathalie
; APPLICANT: BLANCHE, Francis
; APPLICANT: COUZET, Joel
; APPLICANT: BARRIERE, Jean-Claude
; APPLICANT: DEBUSSCHE, Laurent
; APPLICANT: FAMECHON, Alain
; APPLICANT: PARIS, Jean-Marc
; APPLICANT: DUTRUC-ROSSET, Gilles
; TITLE OF INVENTION: Streptogramins And Method For Preparing Same By
; FILE REFERENCE: Streptogramin genes
; CURRENT APPLICATION NUMBER: US/09/987,614A
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US/08/765,907
; PRIOR FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 6
; LENGTH: 4496
; TYPE: DNA
; ORGANISM: Streptomyces pristinaespiralis
US-09-987-614A-6

Query Match 9.4%; Score 111.4; DB 4; Length 4496;
Best Local Similarity 48.5%; Pred. No. 7.1e-27;
Matches 415; Conservative 0; Mismatches 416; Indels 24; Gaps 3;
Qy 249 CATGACCCGCGAAGCATACAAATCCGTTTCAGTCGTGAAACAAAGCCTTTACTCCGCG 308
Db 2027 CATGACCCGCGATGCACCGCACCTCGCGCGCTGCTCAGCCAGGCTTTCACCCCGC 2086
Qy 309 CGTGATGAGCAATGGGACCGAGATTCAGAAATCACAGATGAATCAAAATTT 368
Db 2087 CACCGTCGCCGACCTCGCAACACCGCTCACGAACTGCGCGGCAACTGCTCGACGCGT 2146
Qy 369 TCAGGGCGCAGTGAGTTGACCTTGTTCAGATTTTTCATACCGCTTCGCGTTATTGT 428
Db 2147 CGACGGGACA---CGTTGACCTCTGTCGCGACTTTCGCTTACCGCTGCGCGTATGCT 2203
Qy 429 GATATCTGAGCTGTGGAGTGCTTTCAGCGCAGATGGAAACAGTTTAAAGCATGGTCTGA 488
Db 2204 GATCGCGCAACTCTCTCGCGTGGCGCGCGCGACCCCTGTTTCGCTCTCTGTCGGA 2263
Qy 489 TCTTCTGTCTAGTACACG-----NAGGATAAAGTGAAGCTGA 530
Db 2264 CCGATGCTGAGATGACAGGTGCGCGACCCGCGGACATGCAAGTTTCGCGCAGCAGCGGA 2323
Qy 531 AAAAGCCTTTTGGAAAGACGAGATAGTGTGAGGAGAACTGGCGCGGTTTTTGGCGG 590
Db 2324 CGAGACTTACCAACGCTCTGTCAAAGAACCCATGCGGCGCATGACGCTTACCTCCAGGA 2383

Qy 591 CATCATAGAAAGAAACGAAACAAACCGGAAACAGGATATTTATTTCTATTTTAGTGAAGC 650
Db 2384 CCACGTCACCGACCGCGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2443
Qy 651 GGAAGAAACAGCGGAGAGAGCTGTCGCTGGAAGAGCTGATTCGCTTTTTCACAGCTGCTGCT 710
Db 2444 CCGGTTGAGGGGGAACGACTCACCGACGAGAGAGATCGTCGAATTCGGGGCGCTGCTGCT 2503
Qy 711 GGTGGCGCGGAAATGAAACCACTACAAACCTGATTTCAAATGCGATGTAACAGCATATTAGA 770
Db 2504 GATGGCGCGCCACGTCCTCCACCTCCATGCTGCTCGGCAACACCGTGTGCTGCTGAAGGA 2563
Qy 771 AACGCCAGGCGTTTACGAGGAACCTGCGAGCCATCTGAACTGATGCTCAGGAGTGA 830
Db 2564 CCACCCCGCGCGAGCG 2623
Qy 831 GGAAGCCTTTCGCTTTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 890
Db 2624 AGAAGTACTCGGCTGCG 2683
Qy 891 GGAGATCGGGGGCACCTGATTTAAAGAAAGTGATATGTTTGGCGTTTGTGGCATCGGC 950
Db 2684 CGTCTCGCGCGCACCACTCCCGCGGACGCGATGTCGTGCTGCTGCTGCTGCTGCTGCT 2743
Qy 951 AAATCGTGATGAAGCAAAAGTTTGACAGACCGCACATGTTTGATATTCGCGCGCATCCAA 1010
Db 2744 CAACCCAGCAGCAAGGCTCTTTCACCGACCCCGCGCGCGCGCGCGCGCGCGCGCG 2801
Qy 1011 TCCGATATTCGTTTGGCCACGCGCATCCATTTTTCGCTTGGGGCGCGCGCTGCGCGCT 1070
Db 2802 -CGCAGATCGCTTTCGCT 2860
Qy 1071 TGAAGCAAAATATCGC 1085
Db 2861 GGAGGCCGCGATCGC 2875

RESULT 11

US-09-252-991A-1265
; Sequence 1265, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCES: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1265
; LENGTH: 1314
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1265

Query Match 9.2%; Score 109.8; DB 4; Length 1314;
Best Local Similarity 47.6%; Pred. No. 1e-26;
Matches 422; Conservative 0; Mismatches 432; Indels 33; Gaps 2;
Qy 240 CATCATTAACATGACCGCGCGGAGCATACAAAATTCGTTTCAGTCGTGTAACAAAGCCTT 299
Db 318 CATGCTCAACTCGACCGCGCGGACCATACCCCGCTGCGCTCGCTGCTGCGCGCGGTT 377
Qy 300 TACTCCGCGCGTGATGAAGCAATGGGAACCGAGAAATTCAGAAATCACAGATGAATGAT 359
Db 378 CACCCCGCGCAGTGGAGCGCTGCAACCGCATATAGAACGATCACCGAGGAATGCT 437
Qy 360 TCAAAATTTACGGGGCGCAGTGTGACCTTGTTCAGATTTTTCATACCGCTTCC 419

Db 438 GGAGCCATGGCGCGCGAAGACGGCCGACCTGATGGCCGACTTCGGATCCCGCTGAC 497
Qy 420 GGTATTGTGATATCTGAGCTGCTGGAGTGCCTTCAGGCGAGATGGACAGTTTAAAGC 479
Db 498 CATCGCGTGATCTTCGAGCTGCTGGCAATTCGAGCGCGAGCGCAACACGCCGCGCA 557
Qy 480 ATGGTCTGATCTTCCTGGTCACTACACCGAAGGATAAAGTGAAGCTGTAAGAAAGCCTT 539
Db 558 GTCTGGGAGCGCCAG-----GGGAACTGCTGTC 587
Qy 540 TTTGGAAGACGAGATAAGTGTGAGAGAAATGCGCGCGTGTTCGCGGATCATAGA 599
Db 588 GCGGAGGAGGCCAGGCGCTGCGCGATGCGCAGGTGCACTACCTGCGCTGCTGCTGGA 647
Qy 600 AGAAAGCGAACAACACCGAAGAGATATTTCTATTTTGTAGTGAAGCGGAGAAAC 659
Db 648 GGCCGAAGCGCGCGACCGACCGAGCGTCTACAGCGGCTGGTGCAGCGCCGCGAGA 707
Qy 660 AGGCGAGAGCTGTCGGGTGAAGAGCTGATTCCTGTTTTCAGCGCTGCTGCTGGCGGG 719
Db 708 GAGCGGCCAATGAGGAGCGGAACTCGTCTCCATGGCCCACTGCTGATGATGAGCGG 767
Qy 720 AAATGAACCACTACAAACCTGATTTCAATGCGATGTACAGATATTAGAAACGCCAGG 779
Db 768 CTTGAGACCAACATGATCGGCAACGCGCTGGTCACTCTGCTGCTGCTCAACCCGGA 827
Qy 780 CGTTTACGAGGAACCTGCGCAGCCATCTGAACTGATGCTCAGGCAAGTGGAGAGCCTT 839
Db 828 GCAACTGGCGTTGCTGCGGCGGAGCGGAACTCTGCGCAACGCGCATGAAGAACTGGT 887
Qy 840 GCGTTTCAGAGCGCGCGCCCGCTTTTGAG---GGCAATGCGCAAGCGGATACGAGAT 896
Db 888 CGCCACGACAGCGCGGTCGCGCTCGATGTTGCGCTTCACTGGTGAAGAGCTGGAAC 947
Qy 897 CGGCGGCGACCTGATTAAGAGGTGATATGTTTGGGCTTTGGGCTATGCGCAATCG 956
Db 948 GGACGGGTCACCAATTCGCGCGGCGAATACATCTGCTGCTCAACCTGACCGCAACCA 1007
Qy 957 TCATGAAGCAAGTTTGACAGACCGCACATGTTTGATATCCGCGCATCCCAATCCGCA 1016
Db 1008 CGACGCGGAGCGCTTCGAGATCCGACCGCTCGACCTTACCGCAACACCGATGGCA 1067
Qy 1017 TATTGCGTTTGGCCAGCGCATCCATTTTTCCTTGGGCGCGCTTGGCCGCTTTGAAAGC 1076
Db 1068 TCTCGCTACGCTTCGCGGTGCACTACTGCTGCGGCTCGCTGGCGCGCTGAGGG 1127
Qy 1077 AAATATCGGTTAAAGTCTTTGATTTCTGCTTTTCTCTATATGGAGT 1123
Db 1128 GCGGATCGCCATCCAGCGCTGCTCGCGGCTTCCCGGACCTCCAGT 1174

RESULT 12

US-09-252-991A-1338/c
; Sequence 1338, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1338
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1338

Query Match 9.2%; Score 109.8; DB 4; Length 1482;
Best Local Similarity 47.6%; Pred. No. 1.1e-26;
Matches 422; Conservative 0; Mismatches 432; Indels 33; Gaps 2;
Qy 240 CATATTAAATGACCGCGCGAAGCATACAAATAATCGTTTCAGTCTGTTGAAACAAGCCTT 299
Db 1189 CATGCTCAACTCGACCGCGCGACCATACCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1130
Qy 300 TACTCCGCGTGTATGAAGCAATCGGAACCGAGAAATTCAGAAATACAGATGAATCAT 359
Db 1129 CACCCCGCGCAGGTGAGCGCTTGAACCGCATATAGAACGGATCACCGAGGAATGCT 1070
Qy 360 TCAAAAATTTTCAGGGGCGCAGTGTGACCTTTGTTTTCAGATTTTTCATACCCGCTTCC 419
Db 1069 GGACGCCATGCGCGCGCGAAGCAAGGCGCACTGATGGCCGACTTCGCGATCCCGCTGAC 1010
Qy 420 GGTATTGTGATATCTGAGCTGCTGGAGTGCTTTCAGCGCAGATGGAACAGTTTAAAGC 479
Db 1009 CATCGCGTGTATCTTCGAGCTGCTGGCAATTCGCGAGCGCGAGCGCAACGCCCCGCA 950
Qy 480 ATGCTGTGATCTTCTGCTCAGTACACCGAAGGATAAAGTGAAGAGCTGAAAAAGCCTT 539
Db 949 GTCTGGGAGCGCCAG-----GGGAACTGCTGTC 920
Qy 540 TTTGGAAGACGAGATAAGTGTGAGGAAGAACTGGCCGCGTTCGCGCGCATATAGA 599
Db 919 GCGGAGGAGCGCCAGGCGCTTGGCGGATGCGCAGTTCGACTACCTGCGCTGCTGCTGCA 860
Qy 600 AGAAAGCGAACAACCGGAAACAGGATATTTCTTATTTTGTAGTGAAGCGGAGAAAC 659
Db 859 GGCCAAAGCGCGCGCAGCGCGCGAGCGCTACAGCGGCTGGTGCAGGCGCGCGCAGCA 800
Qy 660 AGGCGAGAGCTGTCGCGTGAAGAGCTGATTCGCTTTTGACGCTGCTGCTGCTGGCGCG 719
Db 799 GAGCGGCACTGAGCGAGCGGAACTCGTCTCCATGCCCCACCTGCTGATGATGAGCGG 740
Qy 720 AAATGAACCACTACAAACCTGATTTCAATGCGATGTACAGATATTAGAAACGCCAGG 779
Db 739 CTTGAGACCACTGAACATGATCGGCAACGCGCTGCTCACCTGCTGCTCAACCCGGA 680
Qy 780 GGTTCAGAGAACTGGCAGCCATCTGAACTGATGCTCAGGCGAGTGGAGGAGCCTT 839
Db 679 GCAACTGCGTGTGCTGCGGCGCGAGAACTCTGCGCAACCGCATGGAAGAACTGCT 620
Qy 840 GCGTTTCAGAGCGCGCGCGCTTTTGAG---GGCAATTCGCAAGCGGAGATACGAGAT 896
Db 619 CGCCACGACAGCGCGTGGCGCTCGATCTTGGCTTTCACCGTGGAGAGCTGGAAC 560
Qy 897 CGGCGGCGCACTGATTAAGAGGTGATATGTTTGGCGTTCGCGATCGGCAATCG 956
Db 559 GGACGGGTCACTTCCCGCGCGAATACATCTGCTCTCAACCTGACCGCGCAACCA 500
Qy 957 TGATGAAGCAAGTTTGACAGACCGCATGTTTGATATCCGCGCATCCCAATCCGCA 1016
Db 499 CGACGCCGAGCGCTTCGACGATCCCGCGCTCGACCTTCCCGCAACCGATGGCA 440
Qy 1017 TATTGCGTTTGGCCACCGCATCCATTTTTCCTTGGGCGCGCTTGGCGCTTCGCGCTTTGAAAGC 1076
Db 439 TCTCGCTACGCTTCGCGCTGCACTACTGCTGCGCGCTCGCTGCGCGCTGAGGG 380
Qy 1077 AAATATCGGTTAAAGTCTTTGATTTTCTGCTTTTCTCTATATGGAGT 1123
Db 379 GCGGATCGCCATCCAGCGCTGCTCGCGGCTTCCCGGACCTCCAGT 333

RESULT 13

US-09-252-991A-1222
; Sequence 1222, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

Qy	923	ATATGGTTTTGGCGCTTTGTGGCATCGGCAATACTGTATGAAGCAAAAGTTTGAACAGACCGC	982
Db	1348	GCCGGGTGGTCGGCTGCTGGGCTCGCGAAACCGGGACCCGGCGCGCTTCCCAGCTCCCG	1407
Qy	983	ACATGTTTGTATATCCGGCGGCATCCCAATTCGCATATATGGCTTTGGCCACGGCATTCATT	1042
Db	1408	ACGTGCTGGACGTCCACCGCGCCCGAAACGGCAGGTGGGTTTCGGCTCGGAATCCACT	1467
Qy	1043	TTTGCCCTTGGGGCCCCCGCTTCCCGTCTTTGAAGCAAAATATCGCGTTAAAGCTCTTTGAT	1100
Db	1468	ACTGCCTCGGCGCAACCTCGCCCGCCGAGGCCGAGATCGTCTCGAGGCGCTGCT	1525

RESIST 15

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RES001.13
US-09-902-540-1222/c
; Sequence 1222, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1222
; LENGTH: 28320
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1222

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Query Match 8.6%; Score 102.6; DB 4; Length 28320;
Best Local Similarity 49.5%; Pred. No. 3.1e-23;
Matches 375; Conservative 0; Mismatches 374; Indels 8; Gaps 4;

Qy	340	GAATC	CAGATG	AATCTG	ATTC	AAATAATTT	CAGGGCG	CAGTGA	GTGTTG	ACCTTG	TTCTAC	399	
Db	2012	GAGAC	CAGCGGG	CTGCTT	GACG	CGCTCG	CGGGCA	AGAACCA	AGTCG	ATCGT	CGGC	1953	
Qy	400	GAATTTT	CATAC	CCCGCTT	CCGGTT	TGTG	TATATCT	GAGTCT	GCTGG	GAGTGC	CTTCAG	459	
Db	1952	GAC	TGGCTT	ACCAATTT	CCCTGT	GACTG	TCATCT	GCAAGT	GCTG	GGAGTCC	CTCGGAG	1893	
Qy	460	CAGATG	GAACAG	TTTAA	AGCATG	GTCTG	TATCTT	CGTCA	GTACAC	CGAAG	GATATAA	AGT	519
Db	1892	GAC	GAAGCG	CGCTTTC	ACGAGT	TGG	CGCGCG	GGCGT	CGAGAC	CCCTTG	TACCC	CAACCA	1833
Qy	520	GAAGA	AGCTG	AAAAAG	CTTTT	TGGA	AGACG	AGATAA	AGTGTG	AGGAAG	AACTT	GGCGCG	579
Db	1832	GGG	ACGAT	CAGCA---	CGNAAG	CCNAG	CGCGAC	CGGAC	GAAGCG	GAGT	GGGCGAG	1776	
Qy	580	TTTTTT	TGCGGC	ATCAT	ATAGA	AAAAAG	CGAAAC	AAACCG	GAAACAG	GATATAT	TATTTCT	PAAT	639
Db	1775	TAC	CTCGT	CGCTCG	CGCGAT	GCCAC	CTG	CGCCAG	CGCGG	CGCGAC	CTGCTC	TCGGG	1716
Qy	640	TTAGT	GGNAG	CGGA	GAAGAA	CAGG	CGAGAG	CTGTCC	GTGAAG	AGCTGAT	TCGTTT	TTCG	699
Db	1715	TTCT	GACG	GNATA	ACGG	CCCCG	AGCGGG	CGGATG	TGCGGG	GAAGAG	GTGTTG	AGCACCG	1656
Qy	700	ACG	CTGCTG	CTGTGT	GCGG	CGAAAT	TGAAC	CACTA	CAAAAC	CTGATTT	CAAAAT	TCGATG	759
Db	1655	CGG	TTGCTG	CTCGT	CGTGG	CCATG	AGAC	CAACCG	CTCAAC	CTCTCG	CCCAAT	TGGCATG	1596
Qy	760	AGC	ATATTAG	NAAAC	CGCCAG	GCGTTT	ACGAG	GAATCT	GCGC	AGCCA	TCTG	GAATG	818
Db	1595	ACC	CTGTG	CGCCAC	ACC	CCGCGT	GTTTG	AGCGG	GTG	CGCGC	GAGCCCC	GAGTGA	1536
Qy	819	TCAGG	CAGT	TGAG	GAAG	ACCTT	TGCGT	TTT	CAGAG	CGCCG	CGCCCG	CTTTG	878